What is claimed is:

1. A method of identifying molecular interaction sites in a target nucleic acid comprising:

comparing the nucleotide sequence of said target nucleic acid with the nucleotide sequences of a plurality of nucleic acids from different taxonomic species;

identifying at least one sequence region which is conserved among said plurality of nucleic acids and said target nucleic acid;

determining whether said conserved region has secondary structure; and

for said conserved region having secondary structure, identifying said secondary structure.

2. The method of claim 1 further comprising identifying at least one structural motif for said conserved region having secondary structure.

3. The method of claim 2 further comprising constructing a set of descriptor elements for said structural motif.

4. The method of claim 3 further comprising identifying further nucleic acids having secondary structures corresponding to said descriptor elements.

5. The method of claim 1 wherein said target nucleic acid is present in a eukaryotic cell.

6. The method of claim 5 wherein said target nucleic acid is selected from the group consisting of mRNA, pre-mRNA, tRNA, rRNA, and snRNA.

7. The method of claim 1 wherein said target nucleic acid is present in a prokaryotic cell.

8. The method of claim 7 wherein said target nucleic acid is RNA.

9. The method of claim 7 wherein said target nucleic acid is bacterial.

10. The method of claim 7 wherein said target nucleic acid is viral.

11. The method of claim 7 wherein said target nucleic acid is from a parasite.

12. The method of claim 1 wherein at least some nucleic acid sequence information is derived from a genetic database.

13. The method of claim 1 wherein said nucleotide sequence of said target nucleic acid is determined by assembling a plurality of expressed sequence tags.

14. The method of claim 1 further comprising comparing said target nucleic acid to paralogous nucleic acids.

15. The method of claim 1 wherein said plurality of nucleic acids from different taxonomic species is obtained by performing a sequence similarity search, an ortholog search, or a combination thereof.

16. The method of claim 1 wherein said plurality of nucleic acids from different taxonomic species is obtained by performing a sequence similarity search and constructing virtual transcripts.

17. The method of claim 1 wherein determining whether said conserved region has secondary structure is performed by self complementarity comparison, alignment and covariance analysis, secondary structure prediction, or a combination thereof.

18. The method of claim 17, wherein said secondary structure comprises at least one bulge, loop, stem, hairpin, knot, triple interact, cloverleaf, or helix.

19. The method of claim 2 wherein said structural motif is identified by performing self complementarity comparison, alignment and covariance analysis, secondary structure prediction, or a combination thereof.

20. The method of claim 3 wherein said set of descriptor elements is constructed using a descriptor database.

21. The method of claim 4 wherein said other nucleic acids having secondary structures corresponding to said descriptor elements are identified by searching at least one database, performing clustering and analysis, searching for orthologs, or a combination thereof.

22. A database containing molecular interaction sites identified by the method of claim 1.

23. The database of claim 22 containing eukaryotic molecular interaction sites.

24. The database of claim 23 containing human molecular interaction sites.

25. The database of claim 22 containing prokaryotic molecular interaction sites.

26. An oligonucleotide comprising a molecular interaction site that is present in the RNA of a selected organism and in the RNA of at least one additional organism, wherein said molecular interaction site serves as a binding site for at least one molecule that when bound to said molecular interaction site modulates the expression of said RNA in said selected organism.

27. An oligonucleotide comprising a molecular interaction site that is present in prokaryotic RNA and in at least one additional prokaryotic RNA, wherein said molecular interaction site serves as a binding site for at least one molecule that when bound to said molecular interaction site modulates the expression of said prokaryotic RNA.

28. The oligonucleotide of claim 27 wherein said molecular interaction site is not present in eukaryotic RNA.

29. The oligonucleotide of claim 27 wherein said molecular interaction site is not present in human RNA.

30. A pharmaceutical composition comprising:

an oligonucleotide comprising a molecular interaction site that is present in a prokaryotic RNA and in at least one additional prokaryotic RNA, wherein said molecular interaction site serves as a binding site for at least one molecule that when bound to said molecular interaction site modulates the expression of said prokaryotic RNA; and

a pharmaceutical carrier or diluent.

31. The pharmaceutical composition of claim 30 wherein said molecular interaction site is not present in eukaryotic RNA.

32. The pharmaceutical composition of claim 30 wherein said molecular interaction site is not present in human RNA.

33. A pharmaceutical composition comprising:

an oligonucleotide comprising a molecular interaction site that is present in the RNA of a selected organism and in the RNA of at least one additional organism, wherein said molecular interaction site serves as a binding site for at least one molecule that when bound to said molecular interaction site modulates the expression of said RNA in said selected organism; and

a pharmaceutical carrier or diluent.

34. A pharmaceutical composition comprising:

an oligonucleotide comprising a molecular interaction site present in a prokaryotic RNA, which site is not present in mamalian RNA; and

a pharmaceutical carrier or diluent.

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